

M.
Brannock

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/581,742A

DATE: 04/17/2002

TIME: 13:02:13

Input Set : A:\P1548R1-US.txt

Output Set: N:\CRF3\04172002\I581742A.raw

ENTERED

RECEIVED

APR 24 2002

TECH CENTER 1600/2900

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3 <110> APPLICANT: de Sauvage, Frederic J.
4   Gurney, Austin
5   Murone, Maximilien
6   Rosenthal, Arnon
7   Stone, Donna M.
8   Wood, William I.
10 <120> TITLE OF INVENTION: Human Suppressor of Fused
12 <130> FILE REFERENCE: P1548R1-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/581,742A
C--> 14 <141> CURRENT FILING DATE: 2000-06-16
14 <150> PRIOR APPLICATION NUMBER: US 60/123,090
15 <151> PRIOR FILING DATE: 1999-03-05
17 <150> PRIOR APPLICATION NUMBER: US 60/135,736
18 <151> PRIOR FILING DATE: 1999-05-25
20 <150> PRIOR APPLICATION NUMBER: PCT/US00/05746
21 <151> PRIOR FILING DATE: 2000-03-02
23 <160> NUMBER OF SEQ ID NOS: 10
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1760
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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33 cagtgcctgc cctacgcacc ccgatggcgg agctgcggcc tagcggcgcc 100
35 cccggcccca ccgcgcccc ccgcccctggc ccgactgccc ccccgccctt 150
37 cgcttcgctc ttccccccgg gactgcacgc catctacgga gagtgcggcc 200
39 gcctttaccc tgaccagccg aacccgctcc aggttaccgc tatcgtcaag 250
41 tactggttg gtggcccaga ccccttgga cttgttagca tgtacaggaa 300
43 tgtggggagc ccttctgcta acatccccga gcaactggac tacatcagct 350
45 tcggcctgag tgatctctat ggtgacaaca gagtccatga gtttacagga 400
47 acagatggac ctagtggttt tggtcttgag ttgaccttc gtctgaagag 450
49 agaaactggg gagtctgccc caccaacatg gcccgagag ttaatgcagg 500
51 gcttggcacg atacgtgttc cagtcagaga acaccttctg cagtggggac 550
53 catgtgtcct ggcacagccc ttgggataac agtgagtcaa gaattcagca 600
55 catgctgctg acagaggacc cacagatgca gcccgtagc acacccttg 650
57 gggtagttac ctctctccag atcgttggtg tctgcaactga agagctacac 700
59 tcagcccagc agtggaacgg gcaggggcatc ctggagctgc tgcggacagt 750
61 gcctattgct ggcggccctt ggctgataac tgacatgcgg aggggagaga 800
63 ccatatttga gatcgatcca cacctgcaag agagagttga caaaggcatc 850
65 gagacagatg gctccaacct gagtgggtgc agtgccaagt gtgcctggga 900
67 tgacctgagc cggccccccg aggatgacga ggacagccgg agcatctgca 950
69 tcggcacaca gccccggcga ctctctggca aagacacaga gcagatccgg 1000
71 gagaccctga ggagaggact cgagatcaac agcaaacctg tccttccacc 1050

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73  aatcaaccct cagcggcaga atggcctcgc ccacgaccgg gccccgagcc 1100
75  gcaaagacag cctggaaaagt gacagctcca cggccatcat tccccatgag 1150
77  ctgattcgca cgcggcagct tgagagcgta catctgaaat tcaaccagga 1200
79  gtccggagcc ctcatctctc tctgcctaag gggcaggctc ctgcatggac 1250
81  ggcactttac atataaaaagt atcacagggtg acatggccat cacgtttgtc 1300
83  tccacgggag tggaaaggcgc ctttgccact gaggagcatc cttacgcggc 1350
85  tcatggaccc tggttacaac tctgaacctc tcctcggagc tctgccctcc 1400
87  cgtcctggaa cgtctttctg ccctgaggag agggtagtca gcatctccaa 1450
89  ttttcagcag ctcaagaacc ttggcccca caggacttcg cagatgtcac 1500
91  attgccctc agtcccctga atgcccttcg gacccaaccc caattcccca 1550
93  agcccctgac cccctagctg ccggggttcc cactcccagt gccacaaccc 1600
95  cctcacctcc cctggcagcc cctcagcgag cctgaggccc agcacccgct 1650
97  ggctccccag cacatggtcc cctcccatgg gctgttgccc agggaaccgg 1700
99  ggcgcggtgg gaacgagctg ctggcctcgg catgtttcaa taaagttgct 1750
101  gtgctgggag 1760
103  <210> SEQ ID NO: 2
104  <211> LENGTH: 431
105  <212> TYPE: PRT
106  <213> ORGANISM: Homo sapiens
108  <400> SEQUENCE: 2
109  Met Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro
110  1 5 10 15
112  Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe
113  20 25 30
115  Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr
116  35 40 45
118  Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr
119  50 55 60
121  Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg
122  65 70 75
124  Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr
125  80 85 90
127  Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His
128  95 100 105
130  Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu
131  110 115 120
133  Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr
134  125 130 135
136  Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln
137  140 145 150
139  Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser
140  155 160 165
142  Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr
143  170 175 180
145  Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val
146  185 190 195
148  Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser
149  200 205 210
151  Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr

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Input Set : A:\P1548R1-US.txt

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```

152          215          220          225
154 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg
155          230          235          240
157 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val
158          245          250          255
160 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser
161          260          265          270
163 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp
164          275          280          285
166 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu
167          290          295          300
169 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly
170          305          310          315
172 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln
173          320          325          330
175 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp
176          335          340          345
178 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu
179          350          355          360
181 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln
182          365          370          375
184 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu
185          380          385          390
187 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala
188          395          400          405
190 Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu
191          410          415          420
193 Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu
194          425          430
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 346
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: consensus DNA used to isolate DNA 33454
204 <220> FEATURE:
205 <221> NAME/KEY: unsure
206 <222> LOCATION: 8, 28, 39, 54-55, 65, 68, 74, 80, 90, 125, 130
207 <223> OTHER INFORMATION: unknown base
209 <400> SEQUENCE: 3
W- 210 ggactgcntg ccatagcggg ttccccgntc ccaccgcgnc cccggcccat 50
W- 212 gccnnaactgc ccccnccgncc ttanacatctn tctttcccan gggactgcac 100
W- 214 gccatctacg gagagtgccg ccgcntttan ccttaccagc cgaacccgct 150
216 ccagggttacc gctatcgta agtactgggt gggtggccca gaccccttgg 200
218 actatgtag catgtacagg aatgtgggga gcccttctgc taacatcccc 250
220 gagcactggc actacatcag cttcggcctg agtgatctct atggtgacaa 300
222 cagagtccat gaagtttaca ggaacagatg gacctagtgg ttttgt 346
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 468

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RAW SEQUENCE LISTING

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226 <212> TYPE: PRT
227 <213> ORGANISM: Drosophila Melanogaster
229 <400> SEQUENCE: 4
230 Met Ala Glu Ala Asn Leu Asp Lys Lys Pro Glu Val Lys Pro Pro
231      1      5      10      15
233 Pro Gly Leu Lys Ala Ile Ile Asp His Leu Gly Gln Val Tyr Pro
234      20      25      30
236 Asn Gln Pro Asn Pro Leu Gln Val Thr Thr Leu Leu Lys Tyr Trp
237      35      40      45
239 Leu Gly Gly Gln Asp Pro Leu Asp Tyr Ile Ser Met Tyr Lys Phe
240      50      55      60
242 Pro Gly Asp Val Asp Arg Asn Val Pro Pro His Trp His Tyr Ile
243      65      70      75
245 Ser Phe Gly Leu Ser Asp Leu His Gly Asp Glu Arg Val His Leu
246      80      85      90
248 Arg Glu Glu Gly Val Thr Arg Ser Gly Met Gly Phe Glu Leu Thr
249      95     100     105
251 Phe Arg Leu Ala Lys Thr Glu Ile Glu Leu Lys Gln Gln Ile Glu
252     110     115     120
254 Asn Pro Glu Lys Pro Gln Arg Ala Pro Thr Trp Pro Ala Asn Leu
255     125     130     135
257 Leu Gln Ala Ile Gly Arg Tyr Cys Phe Gln Thr Gly Asn Gly Leu
258     140     145     150
260 Cys Phe Gly Asp Asn Ile Pro Trp Arg Lys Ser Leu Asp Gly Ser
261     155     160     165
263 Thr Thr Ser Lys Leu Gln Asn Leu Leu Val Ala Gln Asp Pro Gln
264     170     175     180
266 Leu Gly Cys Ile Asp Thr Pro Thr Gly Thr Val Asp Phe Cys Gln
267     185     190     195
269 Ile Val Gly Val Phe Asp Asp Glu Leu Glu Gln Ala Ser Arg Trp
270     200     205     210
272 Asn Gly Arg Gly Val Leu Asn Phe Leu Arg Gln Asp Met Gln Thr
273     215     220     225
275 Gly Gly Asp Trp Leu Val Thr Asn Met Asp Arg Gln Met Ser Val
276     230     235     240
278 Phe Glu Leu Phe Pro Glu Thr Leu Leu Asn Leu Gln Asp Asp Leu
279     245     250     255
281 Glu Lys Gln Gly Ser Asp Leu Ala Gly Val Asn Ala Asp Phe Ser
282     260     265     270
284 Phe Arg Glu Leu Lys Pro Thr Lys Glu Val Lys Glu Glu Val Asp
285     275     280     285
287 Phe Gln Ala Leu Ser Glu Lys Cys Ala Asn Asp Glu Asn Asn Arg
288     290     295     300
290 Gln Leu Thr Asp Thr Gln Met Lys Arg Glu Glu Pro Ser Phe Pro
291     305     310     315
293 Gln Ser Met Ser Met Ser Ser Asn Ser Leu His Lys Ser Cys Pro
294     320     325     330
296 Leu Asp Phe Gln Ala Gln Ala Pro Asn Cys Ile Ser Leu Asp Gly
297     335     340     345

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```

299  Ile Glu Ile Thr Leu Ala Pro Gly Val Ala Lys Tyr Leu Leu Leu
300                      350                      355                      360
302  Ala Ile Lys Asp Arg Ile Arg His Gly Arg His Phe Thr Phe Lys
303                      365                      370                      375
305  Ala Gln His Leu Ala Leu Thr Leu Val Ala Glu Ser Val Thr Gly
306                      380                      385                      390
308  Ser Ala Val Thr Val Asn Glu Pro Tyr Gly Val Leu Gly Tyr Trp
309                      395                      400                      405
311  Ile Gln Val Leu Ile Pro Asp Glu Leu Val Pro Arg Leu Met Glu
312                      410                      415                      420
314  Asp Phe Cys Ser Ala Gly Leu Asp Glu Lys Cys Glu Pro Lys Glu
315                      425                      430                      435
317  Arg Leu Glu Leu Glu Trp Pro Asp Lys Asn Leu Lys Leu Ile Ile
318                      440                      445                      450
320  Asp Gln Pro Glu Pro Val Leu Pro Met Ser Leu Asp Ala Ala Pro
321                      455                      460                      465
323  Leu Lys Met
326 <210> SEQ ID NO: 5
327 <211> LENGTH: 275
328 <212> TYPE: DNA
329 <213> ORGANISM: Mus musculus
331 <400> SEQUENCE: 5
332  gagagtgtcg ccgcctctac cctgaccagc cgaaccgcgt ccaggttacc 50
334  gctatcgta agtactgggtt ggggtgggtccg gacccttggt actatgttag 100
336  catgtacagg aacatgggga gtccttctgc caacatccct gagcactggc 150
338  actacatcag ctttggcctg agtgatctct atgggtgacaa cagagtccat 200
340  gagtttacag gaacagacgg accaagtgga tttggctttg agttgacgtt 250
342  tcgtctgaag agagaaaactg gggag 275
344 <210> SEQ ID NO: 6
345 <211> LENGTH: 23
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: forward PCR cloning primer
352 <400> SEQUENCE: 6
353  cagccgaacc cgctccaggt tac 23
355 <210> SEQ ID NO: 7
356 <211> LENGTH: 25
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: reverse PCR cloning primer
363 <400> SEQUENCE: 7
364  catggactct gttgtcacca tagag 25
366 <210> SEQ ID NO: 8
367 <211> LENGTH: 40
368 <212> TYPE: DNA
369 <213> ORGANISM: Artificial sequence
371 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/17/2002
PATENT APPLICATION: US/09/581,742A TIME: 13:02:14

Input Set : A:\P1548R1-US.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 8,28,39,54,55,65,68,74,80,90,125,130